UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/608,463	06/27/2003	James W. Ryan	JR-10,003-US	6428

25538 7590 05/25/2005

CHERYL H AGRIS PHD
PO BOX 806
PELHAM, NY 10803

EXAMINER	
SLOBODYANSKY, ELIZABETH	
ART UNIT	**PAPER NUMBER**
1652	

DATE MAILED: 05/25/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/608,463	RYAN, JAMES W.	
	Examiner	Art Unit	
	Elizabeth Slobodyansky, PhD	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *03 March 2005*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *7,8,10,12,14-18,20 and 22-31* is/are pending in the application.

4a) Of the above claim(s) *8,12,14,22 and 23* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *7,10,15-18,20 and 24-31* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)

2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *3/3/05*.

4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.

5) ☐ Notice of Informal Patent Application (PTO-152)

6) ☐ Other: _____.

DETAILED ACTION

The amendment filed March 3, 2005 canceling claims 1-6, 9, 11, 13, 19 and 21, amending claims 7, 12, 20 and 22 and adding claims 23-31 has been entered.

Claims 7, 8, 10, 12, 14-18, 20 and 22-31 are pending. Claims 8, 12, 14 and 22 have been previously withdrawn (Office action mailed December 1, 2004, page 3).

Election/Restrictions

Newly submitted claim 23 is directed to an invention that is independent or distinct from the invention originally claimed for the following reasons: while claim 7 and claim 23 are related as product and process of use, these claims are drawn to distinct inventions as explained in the Office action mailed May 6, 2004.

Since applicant has received an action on the merits for the originally presented invention, this invention has been constructively elected by original presentation for prosecution on the merits. Accordingly, claim 23 is withdrawn from consideration as being directed to a non-elected invention. See 37 CFR 1.142(b) and MPEP § 821.03.

Claims 7, 10, 15-18, 20 and 24-31 are under consideration.

Claim Objections

Claim 25 is objected to because of the following: it depends from claim 24 that is drawn to "An isolated nucleic acid molecule". Therefore, claim 25 should recite "The isolated nucleic acid molecule of claim 24" not "sequence of claim 24".

Claim 29 is objected to because of the following: "SSC" is mistyped.

Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 24, 25, 28 and 29 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claim 24 is drawn to a "nucleic acid molecule consisting of at least 20 nucleotides unique to a reverse or forward strand of a contiguous exon-intron region or a contiguous intron-exon region". Thus, it is drawn to any nucleotide sequence, because it is not specified to which sequence an exon-intron and intron-exon regions belong. The specification has support for said regions in SEQ ID NO:4 but not in other sequences.

Claims 25, 28 and 29 recite 20-5000 nucleotides. The specification provides support for the discrete numbers of nucleotides such as 20, 30, 50, 100, ... 5000 (page 3, lines 19-22; page 9, line 34 through page 10, line 2). However, the examiner is unable to locate adequate support in the specification for a fragment of any length that is more than 20 and less than 5000 nucleotides. Thus, there is no indication that exon-intron or intron-exon regions of any genomic sequence as well as fragments of 20-5000

nucleotides of SQ ID NO: 4 were within the scope of the invention as conceived by Applicants at the time the application was filed.

Accordingly, Applicants are required to cancel the new matter in the response to this Office Action.

Claims 7, 10, 15-18, 20 and 24-31 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 7, 10, 15-18, 20, 24-28, 30 and 31, are drawn to a "nucleic acid molecule consisting of at least 20 nucleotides unique to a reverse or forward strand of a non-coding region of SEQ ID NO:4 ...". The specification teaches "Generally, for a probe or primer to be unique in the human genome, it contains at least 14 to16 contiguous nucleotides of a sequence complementary to or identical to a target sequence of interest " (page 3, lines 19-21). And father "The sequence is sufficiently complementary to be able to hybridize with the RNA or DNA, preferably under moderate or high stringency conditions to form a stable duplex or triplex" (page 3, lines 25-27).

Claim 24 is drawn to a "nucleic acid molecule consisting of at least 20 nucleotides unique to a reverse or forward strand of a contiguous exon-intron region or a contiguous intron-exon region" (*Note*: the sequence is not specified).

. Claim 25 depends from claim 24 and is drawn to "nucleic acid molecule [that] is 20-5000 nucleotides in length and contains two nucleotides at the specified positions of SEQ ID NO:4. Thus, claim 24 encompasses any nucleotide sequence and claim 25 is limited to any sequence of 20-5000 nucleotides that hybridizes under unspecified moderate stringency conditions to SEQ ID NO:4. The recitation of nucleotides at the two specific positions of SEQ ID NO:4 practically does not limit the structure of said 20-5000 nucleotides because any two nucleotides can be found in any sequence of 20-5000 nucleotides. It is noted that claim 25 is not drawn to a fragment of SEQ ID NO:4 consisting of 20-5000 nucleotides.

Claim 29 is drawn to "An isolated nucleic acid molecule containing between 20 and 5000 nucleotides or its reverse strand that hybridizes at 55° C", 5xSSC to a non-coding region of SEQ ID NO:4. It is noted that "containing" is open language and the length of the entire molecule as well as the composition of the flanking sequences are not limited.

Thus, claims 7, 10, 15-18, 20 and 24-31 encompass structurally and/or functionally diverse nucleotide molecules.

Therefore, the genus of nucleic acid molecules that comprise these above nucleic acid molecules is a large variable genus with the potentiality of encoding many different proteins and encoding no proteins but having other functions. Therefore, many functionally unrelated nucleic acid molecules are encompassed within the scope of the claim, including partial nucleic acid sequences. The specification does not contain any disclosure of the function of all nucleic acid sequences that hybridize under high

stringency to a non-coding region, including a splice junction of SEQ ID NO:4. There are several known splice variants of SEQ ID NO:4 (Sigalas et al. (1996) Nature medicine, 2, 912-917, especially page 913). The specification discloses only splice sites for a single splice variant of SEQ ID NO:4 from which splice junctions of this variant can be gleaned (page 10, Table 2). Moreover, the specification fails to describe any other representative species by any identifying characteristics or properties and fails to disclose the correlation between the function and structure common to all members of the genus of splice junctions. Thus, one skilled in the art cannot visualize or recognize the identity of the members of the genus.

One skilled in the art cannot reasonably conclude that the applicant had possession of the claimed invention at the time the instant application was filed.

Claims 7, 10, 15-18, 20 and 24-31 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a non-coding region of at least 20 nucleotides or 20-5000 nucleotides of SEQ ID NO:4, does not reasonably provide enablement for at least 20 nucleotides or 20-5000 nucleotides that are unique or hybridize at 55^{o}C, 5xSSC to a non-coding region, including splice junction, i.e. contiguous exon-intron or contiguous intron-exon region, of SEQ ID NO:4 and have no known function. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, how to make and/or use the invention commensurate in scope with these claims.

Factors to be considered in determining whether undue experimentation is required, are summarized in In re Wands 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988). They include (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims.

As explained above, claims 7, 10, 15-18, 20 and 24-31 encompass nucleic acid molecules having different strictures and undefined functions.

While recombinant, mutagenesis and hybridization techniques are known, it is not routine in the art to screen large numbers of nucleic acid molecules wherein the activity is unpredictable based on the instant disclosure. While fragments of SEQ ID NO:4 of at least 20 nucleotides or of 20-5000 nucleotides can be used as probes to identify said sequence or its fragments, the specification does not provide a guidance as to how to use a nucleic acid molecule having the sequence that is "unique" but not necessarily highly homologous to SEQ ID NO:4. Many of the sequences that would hybridize under undefined moderate stringency conditions or at 55^{o}C, 5xSSC have unknown function and cannot be used as probes to identify SEQ ID NO:4.

One of ordinary skill in the art would not know how to use a nucleic acid without knowing its function.

Therefore, one of ordinary skill in the art would require guidance, beyond that provided in the specification, in order to make and use a nucleic acid molecule of at

least 20 nucleotides or of 20-5000 nucleotides that is unique or hybridizes at 55°C, 5xSSC to a non-coding region, including splice junction, i.e. contiguous exon-intron or contiguous intron-exon region, of SEQ ID NO:4 and has no known function in a manner reasonably correlated with the scope of the claims. Without such guidance, the experimentation left to those skilled in the art is undue.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 7, 10, 15-18, 20 and 24-31 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 7, 10, 15-18, 20, 24-28, 30 and 31, are drawn to a "nucleic acid molecule consisting of at least 20 nucleotides unique to a reverse or forward strand of a non-coding region of SEQ ID NO:4 ...". The term "unique" is disclosed by non-limiting examples: "Generally, for a probe or primer to be unique in the human genome, it contains at least 14 to16 contiguous nucleotides of a sequence complementary to or identical to a target sequence of interest " (page 3, lines 19-21). And father "The sequence is sufficiently complementary to be able to hybridize with the RNA or DNA, preferably under moderate or high stringency conditions to form a stable duplex or

triplex" (page 3, lines 25-27). Therefore, the metes and bounds of the term "unique" are unclear.

Claims 7, 10, 15-18, 20, 24 and 26-31 recite "a contiguous exon-intron region or a contiguous intron-exon region". This term is introduced by the amendment of March 3, 2005 to replace the term "splice junction". However, the current terms are not more clear. First, it is unclear what is the difference between exon-intron region or intron-exon region, particularly because either strand may be coding depending on the sequence. Second, both exon-intron and intron-exon region can be construed as comprising the entire genomic sequence. It is different from claiming a fragment of a genomic sequence (SEQ ID NO:4) consisting of X nucleotides that comprises nucleotides 40645-40646, for example. Third, the claims are confusing as reciting a non-coding region that is a contiguous exon containing region.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 7, 10, 15, 24, 26, 27 and 29 are rejected under 35 U.S.C. 102(b) as being anticipated by Muzny et al.

Muzny et al. (GenBank accession AC025423, March 9, 2000) teach the sequence of human chromosome 12 comprising the sequence of SEQ ID NO:4. Said sequence is of at least 20 nucleotides and is unique to a contiguous exon-intron or intron-exon region of SEQ ID NO:4. It would hybridize to its own fragment that is a non-coding region, including an exon-intron or intron-exon region.

Claim 15 is included herein because "A kit" can be construed as a preamble that does not limit the scope and has no patentable weight.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 7, 10, 15-18, 20 and 24-31 are rejected under 35 U.S.C. 103(a) as being unpatentable over Muzny et al. in view of Vogelstein et al.

The teachings of Muzny et al. are outlined above.

Vogelstein et al. (US Patent 5,411,860, GenBank accession NM_002392) teach cloning, functional expression and chromosomal localization of human mouse double minute (MDM2) homolog. They teach cDNA (SEQ ID NO:1) encoding human MDM2 homolog (SEQ ID NO:2) that is 100% identical to the human MDM2 homolog of the

instant invention (SEQ ID NO:2). Using a labeled probe, they localized the gene encoding said human MDM2 homolog to chromosome 12q12-14 (column 5, lines 2-13; the description of SEQ ID NO:1 in the Sequence Listing).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to use said cDNA to identify the genomic DNA that encodes the human MDM2 homolog of SEQ ID NO:2 on chromosome 12q12-14. The motivation is provided by Vogelstein et al. who teach that it binds to oncogene p53 and is diagnostic of tumorogenesis. The state of the art provides various techniques for obtaining genomic DNA using cDNA probes that are usually labeled. The comparison of genomic and cDNA would result in the identification of non-coding regions. One of ordinary skill in the art would have been motivated to use said non-coding regions or fragments thereof of at least 20 nucleotides and up to 5000 nucleotides for detecting variants of chromosome 12q12-14 from genomic nucleotide samples from an individual, for example. As a matter of convenience a non-coding region such as a exon-intron or intron-exon region or fragments thereof can be present in a kit or on a solid support. Further, said support can be a microarray according to a customary use of nucleic acid molecules in the art.

Response to Arguments

Applicant's arguments filed March 3, 2005 have been fully considered but they are not persuasive.

With regard to the 112, 1st paragraph written description rejection, Applicant argues that the rejection is obviated because "the claimed nucleic acid molecule consists of **at least 20 nucleotides unique** to a reverse or forward strand of a non-coding region of SEQ ID NO:4" (Remarks, page 8). This is not persuasive because "unique" as used in the instant application does not mean "identical" and with regard to claim 24, the claimed nucleic acid should not even be unique to SEQ ID NO:4. It is noted that "at least 20 nucleotides" include nucleotide sequences of any length as long as they have 20 or more nucleotides.

With regard to the 112, 1st paragraph enablement rejection, Applicant argues that the amendment of claim 7 obviates the outstanding rejection without giving the reasons for such conclusion (page 9).

With regard to the 112, 2nd paragraph rejection, Applicant argues that the amendment of claim 7 and cancellation of claim 19 obviates the outstanding rejection without giving the reasons for such conclusion (page 9). While the rejection of claim 19 is moot, claim 7 remains rejected for the reasons explained above.

With regard to the 102(b) rejection over Muzny et al., Applicant argues that "as amended, claim 7 is now directed to a nucleic acid molecule consisting of at least 20 nucleotides unique to a non-coding region of SEQ ID NO:4" (page 11). This is not persuasive because "at least 20 nucleotides" include the entire sequence taught by Muzny et al. said sequence comprises exon-intron or intron-exon region. Applicant further argues that "There is no disclosure in Muzny of nucleic acid molecule unique to a non-coding region of SEQ ID NO:4 or particularly an isolated nucleic acid molecule

consisting of at least 20 nucleotides unique to a reverse or forward strand of a contiguous exon-intron region or a contiguous intron-exon region" (page 11). This is not persuasive the sequence is unique to itself including its non-coding region.

The examiner agrees with "Applicant's position that claim 29 would [also] not be anticipated by Muzny et al. since these claims are directed to a 20-5000 nucleotide nucleic acid molecule" (page 12). Indeed, claim 29 is not anticipated.

With regard to the 103(a) rejection, Applicant argues that "Vogelstein et al. merely discloses the cDNA sequence of MDM2; it contains 2372 nucleotides. Muzny et al. discloses the sequences of AC025423 (150,579 nucleotides). Therefore, the cDNA constitutes only 1.6% of the sequence present on AC025423. No direction is provided in these references regarding the genomic organization of the MDM2 gene and particularly, the number and size of exon and intron sequences, location of exon-intron and inton-exon regions and the size of the 5' and 3' noncoding regions. There was also no indication provided in the cited references regarding the position of the noncoding sequences and particularly, contiguous exon-intron or intron-exon regions within AC025423 with respect to the MDM2 gene. Muzny et al. did not recognize that the gene was present in this clone. The human MDM2 genomic sequence was unexpectedly found to contain at least 10 exons. There is a vast range in the size of the introns ranging from 126 bases to about 7 kB. There is also a significant range in the size of the exons, ranging from 51 bases to 573 bases. Again as noted above, no teaching was provided with respect to the size or location of the noncoding or coding sequences of MDM2 within AC025423 " (page 13). This is not persuasive because Muzny et al

disclose the sequence of a human chromosome which should contain genes. Vogelstein et al localized the requisite gene to said chromosome. Further, while "the number and size of exon and intron sequences, location of exon-intron and inton-exon regions and the size of the 5' and 3' noncoding regions" were not disclosed, these references made them obvious. If they were disclosed, it would constitute anticipation.

Applicant further argues that "There are a number of exon and intron sequences that are very small in size (see, for example, introns 25507-25384 (intron 5), 25287-21 169 (intron 6) and exons 2 (36384-36310) and 29565-29615 (exon 4)). It is Applicant's assertion that one of ordinary skill in the art would not have a reasonable expectation of success of actually identifying these particular sequences, particularly, what constitutes intron and exon sequences" (page 14). While these exons and introns are relatively small, there is no reason to believe that one of ordinary skill in the art at the time the invention was made would not localize them using available techniques.

An applicant further argues that "Applicant also notes that there has been a great deal of interest in the scientific community in MDM2 given its potential use as a diagnostic and therapeutic agent. This interest is summarized in the cited patent, Vogelstein et al. However, there was absolutely no disclosure or suggestion of the genomic organization of MDM2 genomic DNA until the instant application was filed. An independent disclosure of the genomic organization of the MDM2 gene was not available until July 21, 2004, more than one year after the filing date of the instant application (Liang et al., 2004, Gene 338:217-223). The Court of Customs and Patent Appeals (CCPA) and its present successor, the Court of Appeals for the Federal Circuit

(CAFC), have held the following considerations to be objective evidence of nonobviousness; long felt need, commercial success, failure of others, copying and unexpected results. In re Sernaker, 702 F.2d 989, 217 U.S.P.Q. 1 (Fed. Cir. 1983); In re Imperato, 179 U.S.P.Q. 710 (CCPA 1973)". This is not persuasive because Applicant does not indicate which of the evidence such as long felt need, commercial success, failure of others, copying or unexpected results, is applicable in this case. Liang et al., *supra*, used previously known techniques to obtain the same results as disclosed in the instant application, i.e.. to localize exons and introns within the genomic sequence.

Applicant argues that "There is no prior art that defines the complete genomic structure of a particular gene" (page 14). If this art would exist, it would be anticipation not obviousness.

Applicants further argue that "A general incentive does not make obvious a particular result, nor does the existence of techniques by which those efforts can be carried out. *In re Deuel* 51 F.3d 1552, 34 U.S.P.Q.2d 1210 (Fed. Cir. 1995). Here, only a general incentive at best was provided" (page 15). This is not persuasive because in *In re Deuel* case, no nucleic acid was known whereas here it is known. The instant invention discloses the specific fragments of a known genomic nucleic acid sequence. The sequences of said fragments were known, the specification teaches the end points of said fragments, i.e. exons and introns. These end points are obvious.

Conclusion

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Elizabeth Slobodyansky, PhD whose telephone number is 571-272-0941. The examiner can normally be reached on M-F 10:00 - 6:30.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapura Achutamurthy, PhD can be reached on 571-272-0928. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

E. Slobodyansky

Elizabeth Slobodyansky, PhD
Primary Examiner
Art Unit 1652

May 19, 2005